



Research Article

Investigation of protists in Momoge wetland (China) through metagenomic next-generation sequencing

Yuting Huang ‡

‡ College of Life Science, Baicheng Normal University, Baicheng, China

Corresponding author: Yuting Huang (huangyuting@bcnu.edu.cn)

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Abstract

The Momoge wetland plays an important role in maintaining the ecosphere and protist is an indispensable component of it. In order to reveal community structure and diversity of protists in Momoge wetland, metagenomic next-generation sequencing (mNGS) was performed. The main results are as follows: 1) A total of 224 species were identified, belonging to 17 phyla, 32 classes, 75 orders, 94 families and 146 genera. Among them, Bacillariophyta, Evosea, Oomycota, Rhodophyta, Ciliophora, Haptophyta, and *Salpingoeca rosetta*, *Guillardia theta*, *Polarella glacialis*, *Cladocopium goreau* were the dominant phyla and species, respectively; 2) Most of them were species adapted to the saline-alkali environment, and the protists of Momoge wetland had higher diversity, fewer dominant species, and higher evenness than those of the harsher environment; 3) KEGG analysis showed that some protistan pathways were related to the saline-alkali environmental adaptation. This research is beneficial to ecological protection and provides valuable information for future studies.

Keywords

protist, biodiversity, Momoge wetland, metagenome

Introduction

The Momoge wetland is located in Zhenlai County, Baicheng City, Jilin Province, China, and its altitude ranges from 130 to 145 m a.s.l. The climate type is temperate continental monsoon, with an average annual temperature of 4.2 °C and an average annual precipitation of 392 mm (Cui et al. 2021). It is a typical saline-alkali wetland (Liu et al. 2022). There are numerous lakes, which are an important habitat for migratory populations of white cranes. It is a significant international wetland, which was also officially listed in The Ramsar Convention's List of Wetlands of International Importance in October 2013 (Cui et al. 2021). The protist is a main link for the transfer of matter (such as carbon and energy of food webs), which sustains primary productivity in aquatic ecosystems (Meira et al. 2018, Cruaud et al. 2019). However, there is little research on protists of the Momoge wetland.

In recent years, metagenomic next-generation sequencing (mNGS) has been employed to provide a comprehensive view of protists in wetlands. For instance, the protistan communities in wetlands were studied to elucidate the dominant species and examine the diversity (Liu et al. 2024, Ogola et al. 2024). Based on mNGS technology, the present study conducted a survey on the composition of protists in Momoge wetland, as well as an analysis of KEGG pathways, aiming to provide information of their diversity and functions.

Material and methods

Sampling and sequencing

Three parallel water samples were collected from Momoge wetland (45°93'N, 123°56'E) (Figure 1) on August, 2024 and filtered through 0.22 µm polycarbonate membranes (Taoyuan, CN). DNA was extracted using Mag-Bind Soil DNA Kit (Omega Bio-tek, USA), and integrity was detected by 1% agarose gel (Thermo, USA). The concentration was measured by Quantus Fluorometer (Promega, USA). Then DNA was fragmented into 350bp by Covaris M220 (Covaris, USA), and NEXTFLEX Rapid DNA-Seq (Bioo Scientific, USA) was used to construct libraries. Illumina NovaSeq 6000 (Illumina, USA) was employed for sequencing in China.Fig. 1

Analysis of data

FASTP v0.20.0 was used for low-quality bases (Q-score≤20) removing (Chen et al. 2018). The reads after quality control were assembled by using MEGAHIT v1.1.2 (Li et al. 2015). CD-HIT v4.6.1 was adopted to cluster the coding sequences to construct the non-redundant gene set (Fu et al. 2012). SOAP v2.21 was used to compare reads with the non-redundant gene set to obtain the abundance information (Li et al. 2008). The sequences of non-redundant gene set were compared to the Non-Redundant Protein Sequence database by using DIAMOND v2.0.13 for species annotation (Buchfink et al. 2021). The package “vegan” of R v4.3.2 was used to calculate the indices of diversity

including Shannon, Simpson, and Pielou's evenness with default parameters (R Core Team 2023). GhostKOALA v3.1 were adopted for KEGG annotation, which were assigned to specific species based on their genes (Kanehisa et al. 2016) and the network diagram was drawn with Gephi v0.10.1 (Bastian et al. 2009).



Figure 1. [doi](#)

The geographic coordinate of the sampling site.

Results

The sequencing results

The total raw and clean data of mNGS were 97.0 and 95.3 Gb, respectively. The results of assembly are shown in Table 1. The raw data have been deposited into the NCBI Sequence Read Archive with BioProject accession number PRJNA1230694.

Table 1.
Summary of assembly.

Sample Name	Contigs Number	Contigs bases (bp)	N50 (bp)	N90 (bp)
Momoge_1	2,690,889	1,449,649,057	523	331
Momoge_2	2,724,190	1,454,135,895	525	331
Momoge_3	2,748,576	1,659,312,158	617	342

The composition and diversity of protists

A total of 17 phyla of protists were identified, corresponding to 32 classes, 75 orders, 94 families, 146 genera, and 224 species (Fig. 2, Suppl. material 1). In the protist community of Momoge wetland, Bacillariophyta (7.55%), Evosea (3.03%), Oomycota (2.81%), Rhodophyta (1.90%), Ciliophora (1.66%), and Haptophyta (1.61%) were the dominant phyla determined by relative abundance, except for others that could not be classified at this level (Fig. 2). As shown in Fig. 3, the percentages of the top species ranked by relative abundance were *Salpingoeca rosetta* (17.99%), *Guillardia theta* (10.32%), *Polarella glacialis* (6.86%), *Cladocopium goreau* (6.35%), *Symbiodinium* sp. CCMP2592 (5.98%), *Symbiodinium natans* (4.95%), *Symbiodinium microadriaticum* (4.92%), *Capsaspora owczarzaki* (4.68%), *Ochromonadaceae* sp. CCMP2298 (2.61%), and *Fragilaria crotonensis* (2.19%).

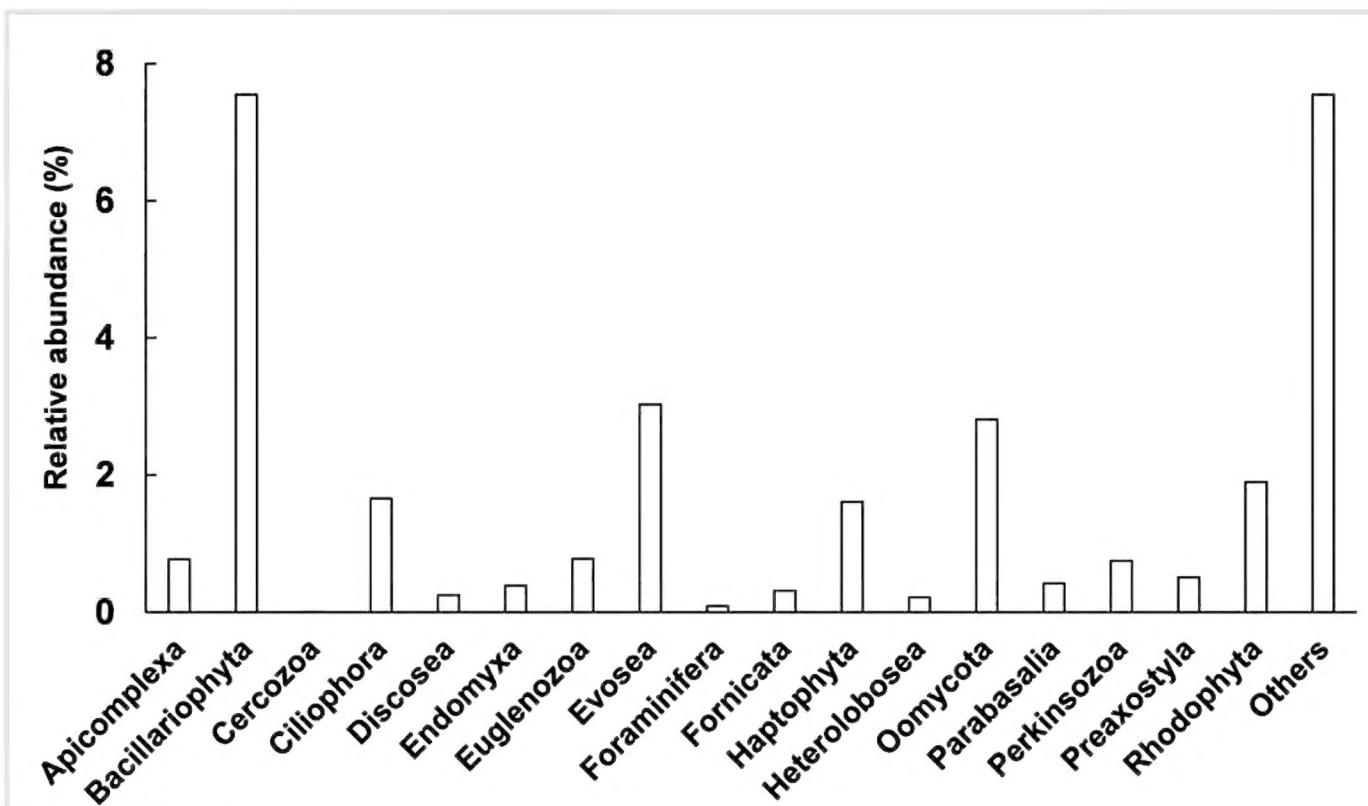


Figure 2. doi

The composition of protists in Momoge wetland. The percentages of relative abundance are at phylum level.

The numbers of species in phyla were shown in Fig. 4 and the species richness of Oomycota, Ciliophora, Euglenozoa, Apicomplexa, Bacillariophyta, Evosea, Rhodophyta, and Haptophyta was higher. The Simpson and Shannon indices were 0.07 and 3.49, respectively (Table 2). In addition, the diversity indices at phylum level are also listed in Table 2. The Oomycota, Euglenozoa, Ciliophora, Apicomplexa, Evosea, Bacillariophyta, Rhodophyta and Haptophyta had higher Shannon indices, while Parabasalia, Perkinsozoa, Rhodophyta, Preaxostyla, Heterolobosea, Fornicata had higher Simpson indices (Table 2). The Pielou's evenness of Heterolobosea was the highest and that of Rhodophyta was the lowest (Table 2).

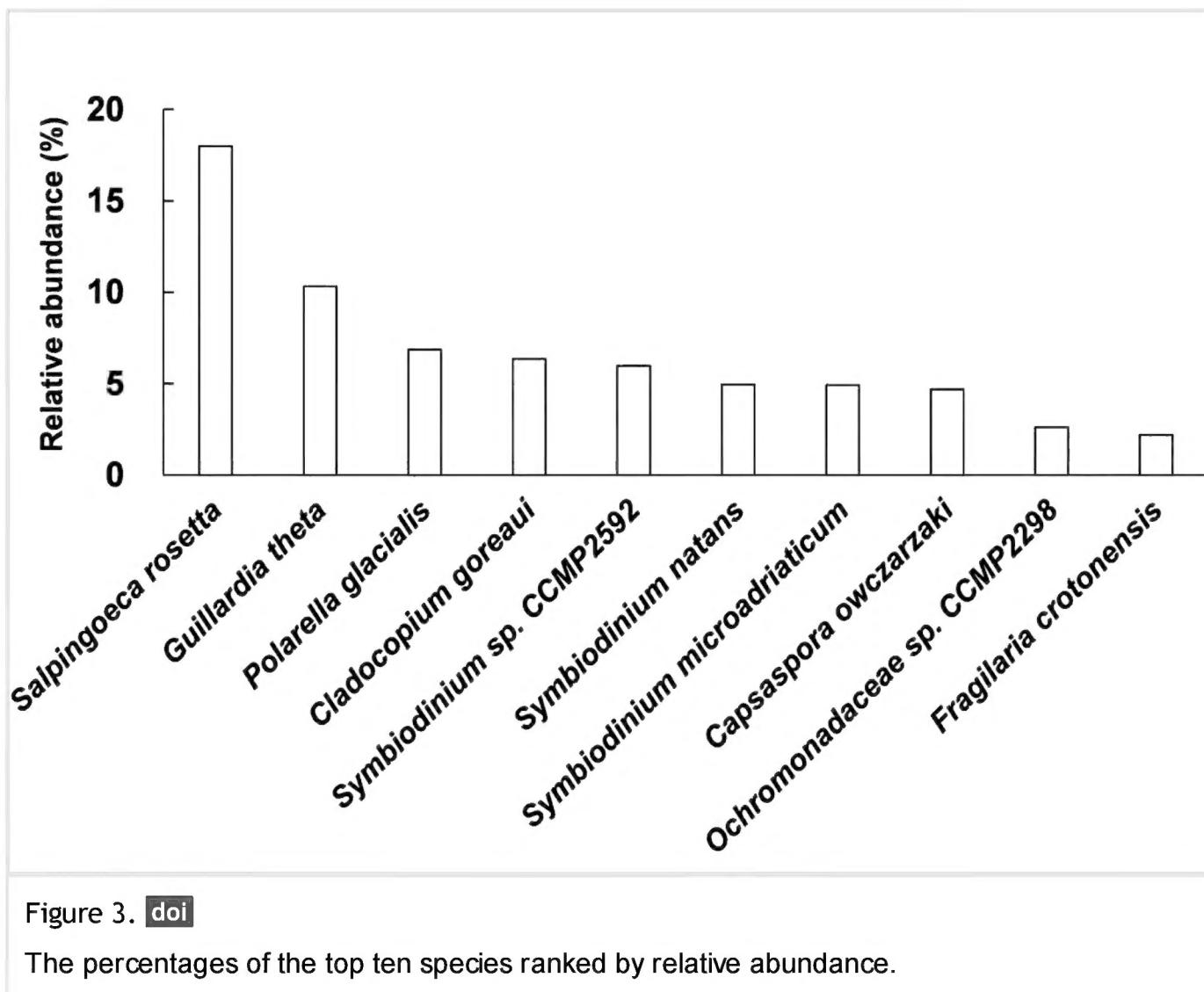


Figure 3. doi

The percentages of the top ten species ranked by relative abundance.

The KEGG network of protists in Momoge wetland

As shown in Fig. 5, the darker the color of pathway category nodes, the greater the number of species involved, and the darker the color of edges, the greater the number of pathways that species participated in under this category. The most annotated genes of species participated in genetic information processing, followed by organismal systems, cellular processes, environmental information processing, and metabolism. The *Anaeramoeba flamelloides* was closely related to cellular processes and environmental information processing. Besides *A. flamelloides*, *G. theta* and *Giardia intestinalis* were highly involved in genetic information processing. Both organismal systems and metabolism were highly associated with *Capsaspora owczarzaki* and *Heterosigma akashiwo*. The details of KEGG pathways are listed in Suppl. material 2.

Table 2.
Diversity indices of protists in Momoge wetland.

Index	All	Apicomplexa	Bacillariophyta	Ciliophora	Euglenozoa	Evosea	Fornicata	Haptophyta	Heterolobosea	Oomycota	Parabasalia	Perkinsozoa	Preaxostyla	Rhodophyta
Shannon index	3.49	2.00	1.98	2.07	1.70	1.98	0.95	1.25	0.94	2.82	0.69	0.78	0.83	1.06
Simpson index	0.07	0.19	0.17	0.18	0.36	0.16	0.42	0.32	0.43	0.09	0.61	0.58	0.52	0.54
Pielou's evenness	0.65	0.72	0.77	0.69	0.57	0.80	0.68	0.78	0.86	0.81	0.63	0.56	0.75	0.46

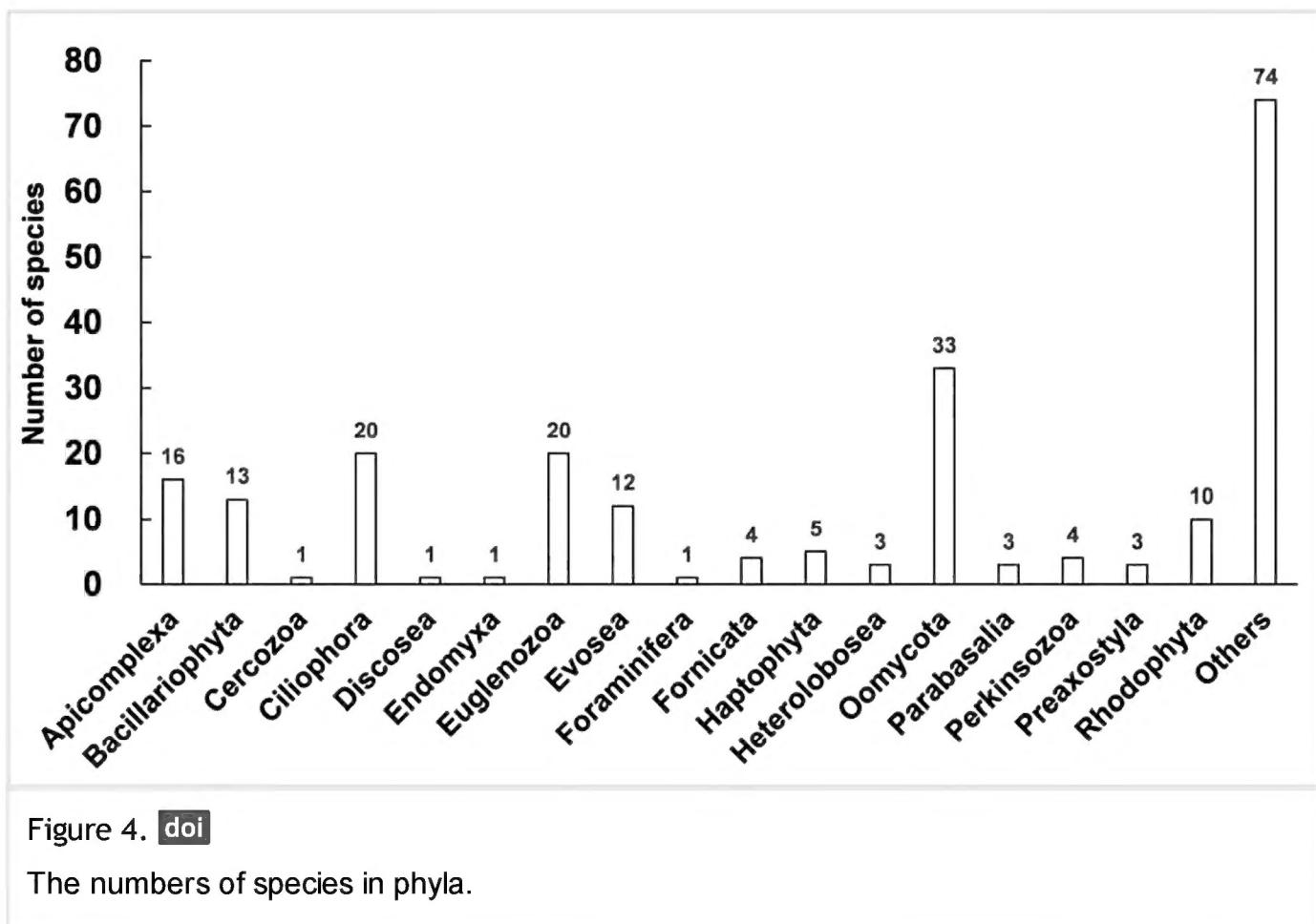


Figure 4. doi

The numbers of species in phyla.

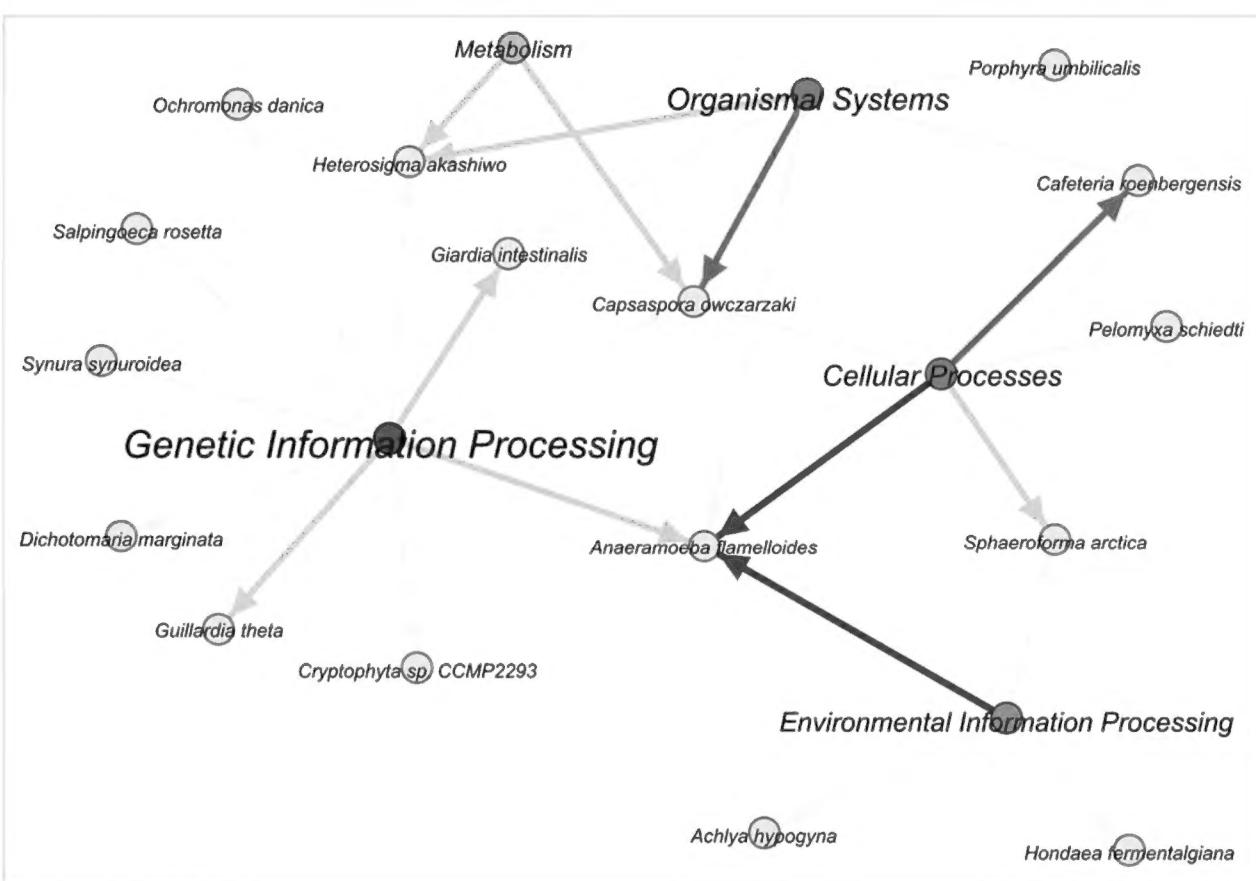


Figure 5. doi

The KEGG network of protists in Momoge wetland. The red and orange nodes: pathway categories; yellow nodes: protists; edges: relations between protists and pathways categories.

Discussion

The community and diversity of protists

The mNGS was performed (Table 1) and Bacillariophyta, Evosea, Oomycota, Rhodophyta, Ciliophora, and Haptophyta were the dominant phyla of the protistan community in Momoge wetland (Fig. 2). The percentages of the dominant species and the diversity indices are also displayed in Fig. 3 and Table 2, respectively. Momoge wetland is a typical saline-alkali wetland (Liu et al. 2022). Diatoms are common components of saline wetlands (Colla et al. 2022), and bacillariophyta (diatom) is the dominant group of autotrophic algae in brackish waters (Mann et al. 2016), which is similar to the result of this study (Figs 2, 4). It has also been found in other saline-alkali wetlands (Zhao et al. 2023). Both *Porphyridium purpureum* and *Galdieria sulphuraria* have the characteristic of salt tolerance (Lu et al. 2020, Abiusi et al. 2021). In this study, they had the higher relative abundance within the Rhodophyta (red algae) (Suppl. material 1). The species richness of Rhodophyta was also high (Fig. 4). Ciliates are dominant components of hypersaline habitats (Harding and Simpson 2018, Weinisch et al. 2019) and both the proportion and species richness of Ciliophora were also relatively high in Fig. 2 and Fig. 4. It is worth noting that *Pseudocohnilembus persalinus*, which is a halophilic ciliate (Weinisch et al. 2019), had the highest relative abundance within the Ciliophora (Suppl. material 1). Although Heterolobosea is also halophilic (Harding and Simpson 2018), its relative abundance was not high in this study (Fig. 2), and the reason needs to be investigated. As for Haptophyta (Suppl. material 1), *Emiliania huxleyi* tolerates a broad range of salinity conditions (Sheward et al. 2024). *S. rosetta*, as the top specie in Momoge wetland (Fig. 3), has close relatives that are highly adapted to the hypersaline environment (Schiwitza et al. 2018). *Guillardia* of Cryptophyta has high relative abundance in salt lake (Yang et al. 2024). In this study, the relative abundance of *G. theta* within the same genus was also high (Fig. 3). It has been reported that filasterean *C. owczarzaki*, which has high relative abundance as shown in Fig. 3, can respond to osmotic stress conditions (Shabardina et al. 2023). These results in the present study indicate that most of the dominant protists were those adapted to saline-alkali environment. In addition, both Evosea and Oomycetes can degrade organisms (Thines 2018, Bosch et al. 2024). Their high relative abundances and species richness (Figs 2, 4) as well as the high Shannon index of Oomycetes (Table 2) suggest that they were main consumers of saprophytic nutrients in Momoge wetland. The Shannon, Simpson, and Pielou's indices measure the species diversity, dominance, and evenness of a community, respectively (Shannon 1948, Simpson 1949, Pielou 1966). In the present study, the Shannon index, Simpson index, and Pielou's evenness of protists were 3.49, 0.07, and 0.65 (Table 2), while these indices are 2.93, 0.15, and 0.56 in Tibetan Plateau's wetland (Zhang et al. 2022). It can be seen that compared to those of Tibetan Plateau's wetland, protists of Momoge wetland had higher diversity, fewer dominant species, and higher evenness. This might be due to the harsher environment of the plateau. Moreover, the dominant phyla also demonstrated higher Shannon indices generally, which means that they were the main contributors to the total value of Shannon (Fig. 2, Table 2).

However, the values of Simpson and Pielou's evenness (Fig. 2, Table 2) suggested that the composition of species in some dominant ones was not as uniform as that in others.

The KEGG functions of protists

The network between species and KEGG pathways was constructed (Fig. 5, Suppl. material 2). As seen from the graph, the *A. flamelloides* was closely connected with cellular processes and environmental information processing. It is an anaerobic organism (Åberg 2024), and there are currently no reports that it tolerates saline-alkali conditions. According to Suppl. material 2, it participated in KEGG pathways such as cellular senescence, FoxO signaling pathway, PI3K-Akt signaling pathway, Wnt signaling pathway, Hedgehog signaling pathway, Hippo signaling pathway, JAK-STAT signaling pathway. These pathways mainly maintain normal physiological functions such as development (Rawlings et al. 2004, Evangelista et al. 2006, Pan 2010, Jafari et al. 2019, Hayat et al. 2022). In addition, the relations between genetic information processing, organismal systems, metabolism and *G. theta*, *G. intestinalis*, *C. owczarzaki*, as well as *H. akashiwo*, were also close (Fig. 5). As mentioned above, *Guillardia* has been found in salt lake (Yang et al. 2024) and the osmotolerance contractile vacuole is also in *G. theta* (Hoef-Emden 2014). Its KEGG pathways of genetic information processing were protein processing in endoplasmic reticulum and basal transcription factors (Suppl. material 2). Whether these pathways are related to the formation of contractile vacuoles requires further verification. The KEGG pathways of filasterean *C. owczarzaki* were glycosylphosphatidylinositol (GPI)-anchor biosynthesis, SNARE interactions in vesicular transport, endocytosis and so on (Suppl. material 2). It has been reported that phosphatidylinositol signaling, SNARE proteins, endocytosis are related to the salt tolerance of eukaryotes (Salinas-Cornejo et al. 2021, Salinas-Cornejo et al. 2023, Yang et al. 2024). As for *H. akashiwo*, its main KEGG pathways were oxidative phosphorylation, thermogenesis, and retrograde endocannabinoid signaling (Suppl. material 2). Except for that, the heterotrophic nanoflagellates *Cafeteria roenbergensis* (De Corte et al. 2019) also participated in cellular processes quite a lot (Fig. 5) and its main KEGG pathways included apoptosis, antigen processing and presentation, autophagy, lysosome, and phagosome (Suppl. material 2). Similarly, these pathways were identified in the KEGG analysis of other eukaryotic organisms under saline-alkali environments (Shi et al. 2023, Jin et al. 2024, Wang et al. 2025).

Conclusions

In summary, this research accomplished investigation of protists in Momoge wetland. Based on mNGS technology, the dominant phyla and species were identified and the diversity indices were also calculated. The analyses revealed the KEGG functions of protists as well. In detail, the Bacillariophyta, Evosea, Oomycota, Rhodophyta, Ciliophora, Haptophyta, *S. rosetta*, *G. theta*, *P. glacialis*, and *C. goreau* were the dominant ones in Momoge wetland and most of them are adapted to the saline-alkali environment. The protists in Momoge wetland had higher diversity, fewer dominant species, and higher evenness than those in harsher environment. Some KEGG pathways of *A. flamelloides*,

G. theta, *G. intestinalis*, *C. owczarzaki*, *H. akashiwo*, and *C. roenbergensis* were involved in normal physiology, while some were related to the saline-alkali environment's adaptation. As shown in the present study, compared to traditional approaches, the mNGS is culture-free and it can obtain functional annotations. The information regarding protists in Momoge wetland will be beneficial for the maintenance and protection of ecological diversity, as well as future studies.

Acknowledgements

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Conflicts of interest

The author declare no conflict of interest.

References

- Åberg O (2024) Exploring the anaerobic protist *Anaeramoeba flamelloides*: Culturing methodology, cell structure imaging, antibiotic assay and symbiont genomics. Uppsala University.
- Abiusi F, Trompeter E, Hoenink H (2021) Autotrophic and mixotrophic biomass production of the acidophilic *Galdieria sulphuraria* ACUF 64. Algal Research 60 (12): 102513. <https://doi.org/10.1016/j.algal.2021.102513>
- Bastian M, Heymann S, Jacomy M (2009) Gephi: an open source software for exploring and manipulating networks. Proceedings of the international AAAI conference on web and social media 3(1). 361-362 pp. <https://doi.org/10.1609/icwsm.v3i1.13937>
- Bosch J, Dobbler PT, Větrovský T, Tláskal V, Baldrian P, Brabcová V (2024) Decomposition of *Fomes fomentarius* fruiting bodies—transition of healthy living fungus into a decayed bacteria-rich habitat is primarily driven by Arthropoda. FEMS Microbiology Ecology 100 (5): fiae044. <https://doi.org/10.1093/femsec/fiae044>
- Buchfink B, Reuter K, Drost H (2021) Sensitive protein alignments at tree-of-life scale using DIAMOND. Nature Methods 18 (4): 366-368. <https://doi.org/10.1038/s41592-021-01101-x>
- Chen S, Zhou Y, Chen Y, Gu J (2018) fastp: an ultra-fast all-in-one FASTQ preprocessor. Bioinformatics 34 (17): i884-i890. <https://doi.org/10.1093/bioinformatics/bty560>
- Colla MF, Lencina AI, Farías ME (2022) Diatom and invertebrate assemblages in high altitude saline wetlands of the Argentinian Puna and their relation to environmental factors. Anais da Academia Brasileira de Ciências 94 (1). <https://doi.org/10.1590/0001-3765202220200070>
- Cruaud P, Vigneron A, Fradette M, Dorea CC, Culley AI, Rodriguez MJ, Charette SJ (2019) Annual protist community dynamics in a freshwater ecosystem undergoing

- contrasted climatic conditions: The Saint-Charles River (Canada). *Frontiers in Microbiology* 10: 2359. <https://doi.org/10.3389/fmicb.2019.02359>
- Cui G, Liu Y, Tong S (2021) Analysis of the causes of wetland landscape patterns and hydrological connectivity changes in Momoge National Nature Reserve based on the Google Earth Engine Platform. *Arabian Journal of Geosciences* 14 (3): 170. <https://doi.org/10.1007/s12517-021-06568-8>
 - De Corte D, Paredes G, Yokokawa T, Sintes E, Herndl GJ (2019) Differential response of *Cafeteria roenbergensis* to different bacterial and archaeal prey characteristics. *Microbial Ecology* 78: 1-5. <https://doi.org/10.1007/s00248-018-1293-y>
 - Evangelista M, Tian H, de Sauvage FJ (2006) The hedgehog signaling pathway in cancer. *Clinical Cancer Research* 12 (20): 5924-5928. <https://doi.org/10.1158/1078-0432.CCR-06-1736>
 - Fu L, Niu B, Zhu Z, Wu S, Li W (2012) CD-HIT: accelerated for clustering the next-generation sequencing data. *Bioinformatics* 28 (23): 3150-3152. <https://doi.org/10.1093/bioinformatics/bts565>
 - Harding T, Simpson AG (2018) Recent advances in halophilic protozoa research. *Journal of Eukaryotic Microbiology* 65 (4): 556-570. <https://doi.org/10.1111/jeu.12495>
 - Hayat R, Manzoor M, Hussain A (2022) Wnt signaling pathway: A comprehensive review. *Cell Biology International* 46 (6): 863-877. <https://doi.org/10.1002/cbin.11797>
 - Hoef-Emden K (2014) Osmotolerance in the Cryptophyceae: Jacks-of-all-trades in the Chroomonas Clade. *Protist* 165 (2): 123-143. <https://doi.org/10.1016/j.protis.2014.01.001>
 - Jafari M, Ghadami E, Dadkhah T, Akhavan-Niaki H (2019) PI3k/AKT signaling pathway: Erythropoiesis and beyond. *Journal of Cellular Physiology* 234 (3): 2373-2385. <https://doi.org/10.1002/jcp.27262>
 - Jin S, Zhou R, Gao X, et al. (2024) Identification of the effects of alkalinity exposure on the gills of oriental river prawns, *Macrobrachium nipponense*. *BMC genomics* 25 (1): 765. <https://doi.org/10.1186/s12864-024-10659-7>
 - Kanehisa M, Sato Y, Kawashima M, Furumichi M, Tanabe M (2016) KEGG as a reference resource for gene and protein annotation. *Nucleic Acids Research* 44 (D1): D457-D462. <https://doi.org/10.1093/nar/gkv1070>
 - Li D, Liu C, Luo R, Sadakane K, Lam T (2015) MEGAHIT: an ultra-fast single-node solution for large and complex metagenomics assembly via succinct de Bruijn graph. *Bioinformatics* 31 (10): 1674-1676. <https://doi.org/10.1093/bioinformatics/btv033>
 - Li R, Li Y, Kristiansen K, Wang J (2008) SOAP: short oligonucleotide alignment program. *Bioinformatics* 24 (5): 713-714. <https://doi.org/10.1093/bioinformatics/btn025>
 - Liu F, Ding J, Zeng J, Wang C, Wu B, Yan Q, He Z, Shu L (2024) Mangrove sediments are environmental hotspots for pathogenic protists. *Journal of Hazardous Materials* 467: 133643. <https://doi.org/10.1016/j.jhazmat.2024.133643>
 - Liu Y, Cui G, Tong S, et al. (2022) Determination of the hydrodynamic characteristics of a typical inland saline-alkali wetland in Northeast China. *Frontiers in Ecology and Evolution* 10: 939431. <https://doi.org/10.3389/fevo.2022.939431>
 - Lu X, Nan F, Feng J, et al. (2020) Effects of different environmental factors on the growth and bioactive substance accumulation of *Porphyridium purpureum*. *International journal of environmental research and public health* 17 (7): 2221. <https://doi.org/10.3390/ijerph17072221>
 - Mann D, Crawford R, Round F (2016) Bacillariophyta. In: Archibald J, Simpson AB, Slamovits C, Margulis L, Melkonian M, Chapman D, Corliss J (Eds) *Handbook of the*

- Protists. Springer International Publishing, Cham, 61 pp. https://doi.org/10.1007/978-3-319-32669-6_29-1
- Meira BR, Lansac-Toha FM, Segovia BT, Buosi PRB, Lansac-Tôha FA, Velho LFM (2018) The importance of herbivory by protists in lakes of a tropical floodplain system. *Aquatic Ecology* 52: 193-210. <https://doi.org/10.1007/s10452-018-9654-7>
 - Ogola HJO, Ijoma GN, Edokpayi JN (2024) Exploring the dichotomy: Shotgun metagenomics reveals diversity of beneficial and pathogenic protist community in arid wetlands of northeastern South Africa. *Science of the Total Environment* 946: 174306. <https://doi.org/10.1016/j.scitotenv.2024.174306>
 - Pan D (2010) The hippo signaling pathway in development and cancer. *Developmental cell* 19 (4): 491-505. <https://doi.org/10.1016/j.devcel.2010.09.011>
 - Pielou EC (1966) The measurement of diversity in different types of biological collections. *Journal of theoretical biology* 13: 131-144. [https://doi.org/10.1016/0022-5193\(66\)90013-0](https://doi.org/10.1016/0022-5193(66)90013-0)
 - Rawlings JS, Rosler KM, Harrison DA (2004) The JAK/STAT signaling pathway. *Journal of Cell Science* 117 (8): 1281-1283. <https://doi.org/10.1242/jcs.00963>
 - R Core Team (2023) R: A language and environment for statistical computing. R Foundation for Statistical Computing. URL: <https://www.R-project.org/>
 - Salinas-Cornejo J, Madrid-Espinoza J, I V (2021) The exocytosis associated SNAP25-type protein, SISNAP33, increases salt stress tolerance by modulating endocytosis in tomato. *Plants* 10 (7): 1322. <https://doi.org/10.3390/plants10071322>
 - Salinas-Cornejo J, Madrid-Espinoza J, I V (2023) A SNARE-like protein from Solanum lycopersicum increases salt tolerance by modulating vesicular trafficking in tomato. *Frontiers in Plant Science* 14: 1212806. <https://doi.org/10.3389/fpls.2023.1212806>
 - Schiwitza S, Arndt H, Nitsche F (2018) Four new choanoflagellate species from extreme saline environments: Indication for isolation-driven speciation exemplified by highly adapted Craspedida from salt flats in the Atacama Desert (Northern Chile). *European Journal of Protistology* 66: 86-96. <https://doi.org/10.1016/j.ejop.2018.08.001>
 - Shabardina V, Charria PR, GB S (2023) Evolutionary analysis of p38 stress-activated kinases in unicellular relatives of animals suggests an ancestral function in osmotic stress. *Open Biology* 13 (1): 220314. <https://doi.org/10.1098/rsob.220314>
 - Shannon CE (1948) A mathematical theory of communication. *The Bell system technical journal* 27 (3): 379-423. <https://doi.org/10.1002/j.1538-7305.1948.tb01338.x>
 - Sheward RM, Gebühr C, Bollmann J, Herrle JO (2024) Short-term response of *Emiliania huxleyi* growth and morphology to abrupt salinity stress. *Biogeosciences* 21 (13): 3121-3141. <https://doi.org/10.5194/bg-21-3121-2024>
 - Shi X, Zhang R, Liu Z, et al. (2023) Combined analysis of mRNA and miRNA reveals the mechanism of pacific white shrimp (*Litopenaeus vannamei*) under acute alkalinity stress. *PLoS one* 18 (8): e0290157. <https://doi.org/10.1371/journal.pone.0290157>
 - Simpson EH (1949) Measurement of diversity. *nature* 163 (4148): 688-688. <https://doi.org/10.1038/163688a0>
 - Thines M (2018) Oomycetes. *Current Biology* 28 (15): R812-R813. <https://doi.org/10.1016/j.cub.2018.05.062>
 - Wang J, Jiang X, Mu C, et al. (2025) Transcriptomic insights into the adaptive mechanisms of antennal glands in mud crab (*Scylla paramamosain*) to acute chloride-type low-salinity alkaline water stress. *Journal of Oceanology and Limnology* 1-13. <https://doi.org/10.1007/s00343-025-4331-x>

- Weinisch L, Kirchner I, Grimm M, et al. (2019) Glycine betaine and ectoine are the major compatible solutes used by four different halophilic heterotrophic ciliates. *Microbial ecology* 77 (2): 317-331. <https://doi.org/10.1007/s00248-018-1230-0>
- Yang J, Wang C, Wang Z, et al. (2024) Distribution patterns and co-occurrence network of eukaryotic algae in different salinity waters of Yuncheng Salt Lake, China. *Scientific Reports* 14: 8340. <https://doi.org/10.1038/s41598-024-58636-0>
- Yang L, Wang Y, Bai Y, et al. (2024) Lipid metabolism improves salt tolerance of *Salicornia europaea*. *Annals of Botany*. mcae189 pp. <https://doi.org/10.1093/aob/mcae189>
- Zhang P, Xiong J, Qiao N, et al. (2022) Spatiotemporal distribution of protists in the Yarlung Zangbo River, Tibetan plateau. *Water Biology and Security* 1 (4): 100064. <https://doi.org/10.1016/j.watbs.2022.100064>
- Zhao Z, Song T, Zhang M, et al. (2023) Benefits of Morphology-Based Functional Group Classification to Study Dynamic Changes in Phytoplankton in Saline-Alkali Wetlands, Taking Typical Saline-Alkali Wetlands in Northeast China as an Example. *Diversity* 15 (12): 1175. <https://doi.org/10.3390/d15121175>

Supplementary materials

Suppl. material 1: Table S1 [doi](#)

Authors: Yuting Huang

Data type: table

Brief description: The classification of protists in Momoge wetland

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Suppl. material 2: Table S2 [doi](#)

Authors: Yuting Huang

Data type: table

Brief description: KEGG pathways of protists in Momoge wetland

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